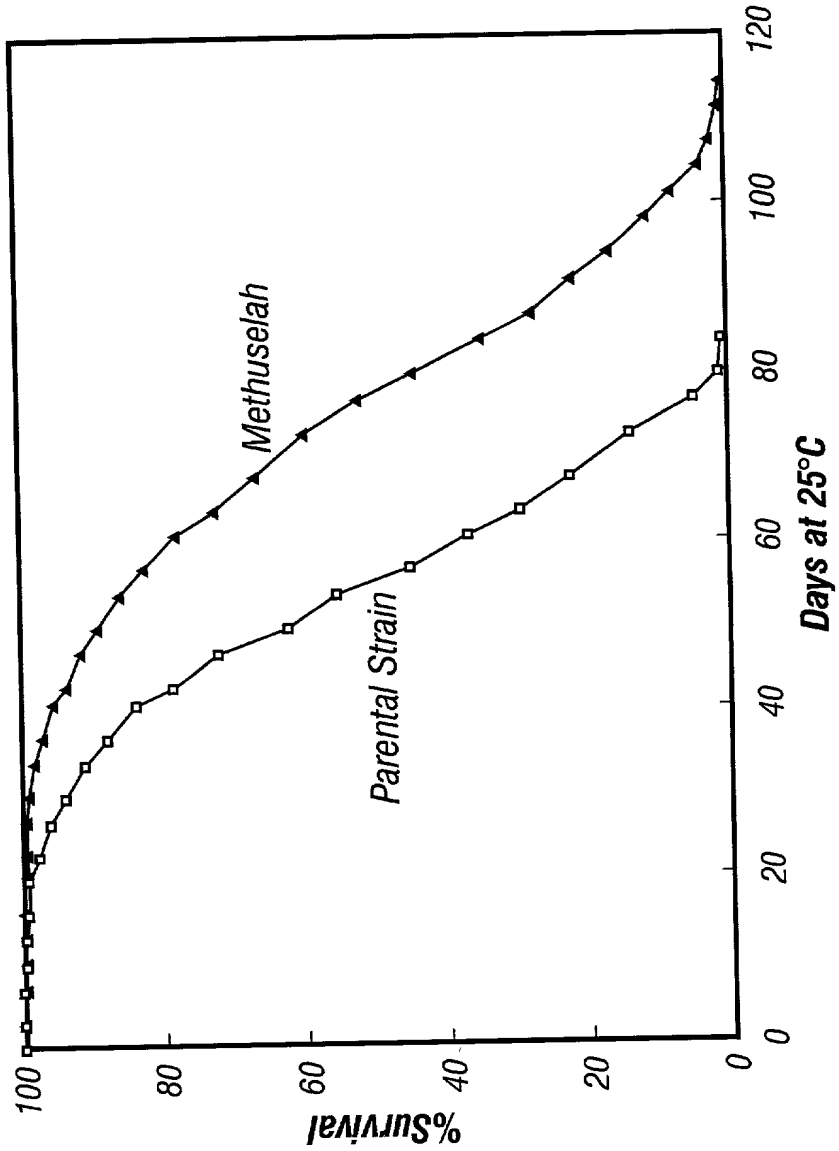
%Survival
100
80
60
40
20
0
0
20
40
60
80
100
120
Days at 25°C
Methuselah
Parental Strain

FIG. 1

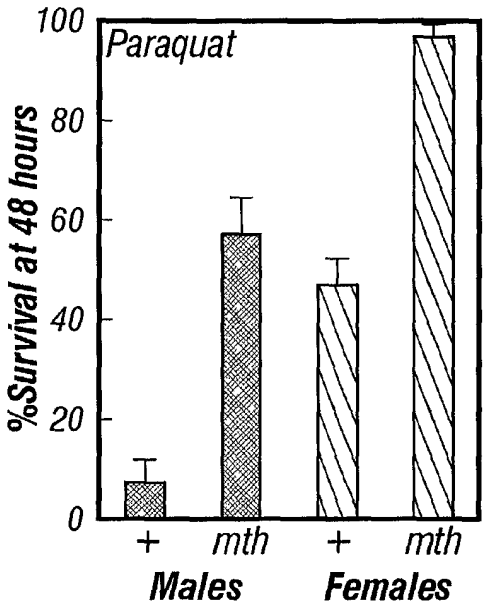

FIG. 2A

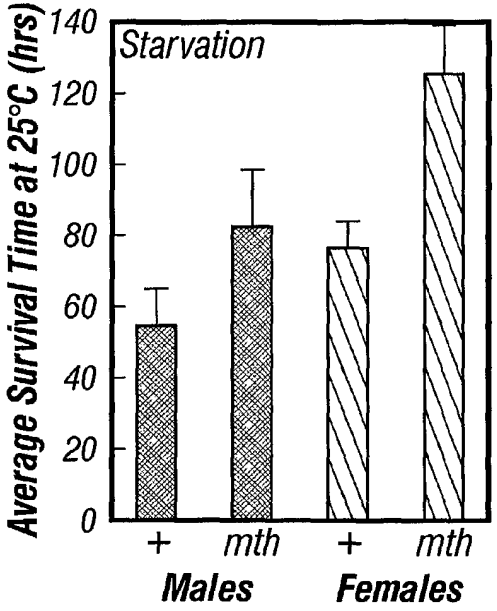

FIG. 2B

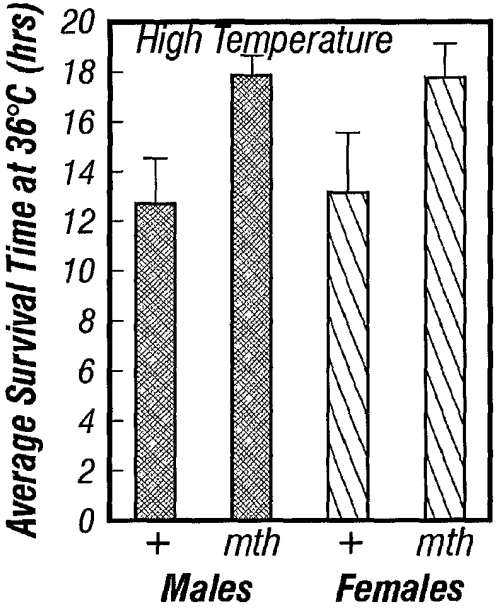

FIG. 2C

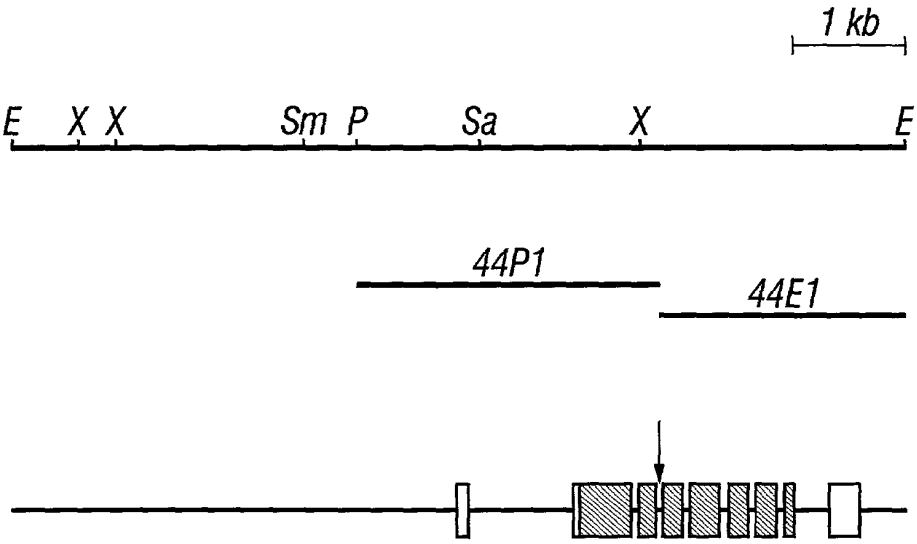
1 kb
E X X Sm P Sa X E
44P1
44E1

FIG. 3A

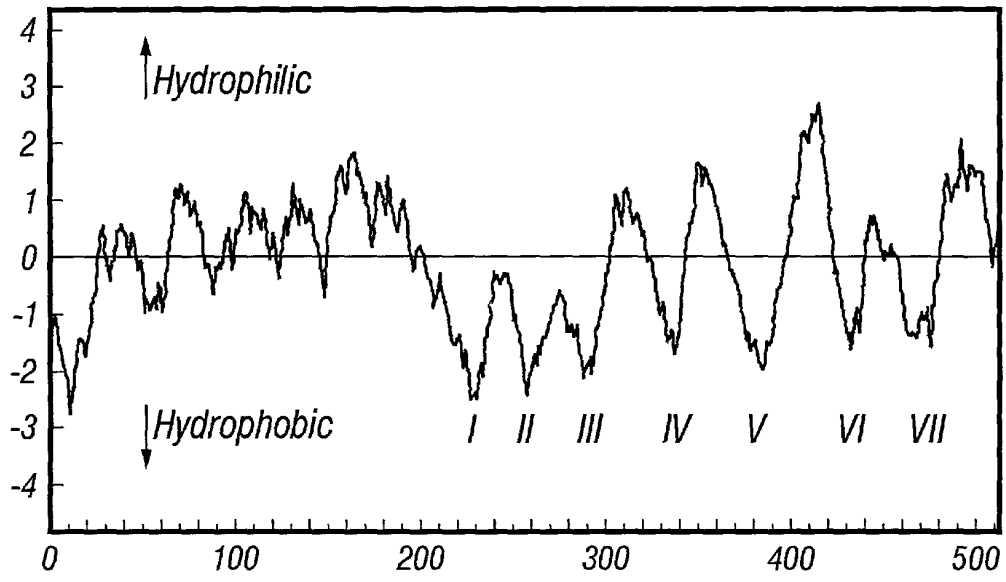
4
3
2
1
0
-1
-2
-3
-4
Hydrophilic
Hydrophobic
I II III IV V VI VII
0 100 200 300 400 500

FIG. 3C

```
1    TAAAGTTTAGTTGTCACACACATCTGTGTGAGTTTTAAGCTTAAAAAGTTCAAACGCGGAACGTCCATGTCCGCTTG
80   ATACAGAACGTCCATGTCCGCTTGATACACCGATCGAGAACAAAAAGCATAA              ATG AAA ACT CTT
                                                                        M   K   T   L     4
121  TTG GTT CTT CGG ATA TCA ACT GTC ATA CTT GTT GTG CTG GTT ATT CAA AAA TCA TAT GCA
      L   V   L   R   I   S   T   V   I   L   V   V   L   V   I   Q   K   S   Y   A     24
181  GAC ATT CTC GAA TGC GAT TAT TTC GAC ACT GTC GAT ATT TCG GCA GCT CAA AAA CTA CAG
      D   I   L   E   C   D   Y   F   D   T   V   D   I   S   A   A   Q   K   L   Q     44
241  AAT GGA TCG TAC TTA TTT GAG GGG TTG CTC GTT CCG GCC ATT TTG ACG GGA GAA TAT GAC
      N   G   S   Y   L   F   E   G   L   L   V   P   A   I   L   T   G   E   Y   D     64
301  TTT AGG ATT CTC CCG GAC GAC TCG AAG CAG AAG GTG GCT CGT CAC ATA AGA GGA TGT GTG
      F   R   I   L   P   D   D   S   K   Q   K   V   A   R   H   I   R   G   C   V     84
361  TGC AAG CTG AAG CCC TGT GTC AGA TTT TGC TGC CCT CAC GAC CAT ATC ATG GAT AAT GGT
      C   K   L   K   P   C   V   R   F   C   C   P   H   D   H   I   M   D   N   G    104
421  GTC TGC TAC GAC AAC ATG TCC GAC GAG GAG CTG GCT GAA CTC GAT CCC TTC CTT AAT GTG
      V   C   Y   D   N   M   S   D   E   E   L   A   E   L   D   P   F   L   N   V    124
481  ACT CTT GAC GAC GGG TCG GTG TCC CGC AGA CAC TTT AAA AAC GAA CTA ATC GTC CAG TGG
      T   L   D   D   G   S   V   S   R   R   H   F   K   N   E   L   I   V   Q   W    144
541  GAC CTA CCG ATG CCG TGT GAC GGA ATG TTC TAC CTA GAC AAC CGC GAA GAA CAG GAT AAG
      D   L   P   M   P   C   D   G   M   F   Y   L   D   N   R   E   E   Q   D   K    164
601  TAC ACG TTG TTC GAG AAC GGA ACT TTC TTT CGC CAC TTT GAC CGT GTG ACT CTT CGC AAG
      Y   T   L   F   E   N   G   T   F   F   R   H   F   D   R   V   T   L   R   K    184
661  CGG GAA TAC TGC CTT CAG CAT CTT ACA TTC GCA GAT GGT AAT GCT ACG TCT ATT CGA ATT
      R   E   Y   C   L   Q   H   L   T   F   A   D   G   N   A   T   S   I   R   I    204
721  GCA CCT CAC AAC TCT TTG ATA GTG CCA TCA ATT ACC GGT CAG ACG GTT GTG ATG ATC TCT
      A   P   H   N   C   L   I   V   P   S   I   T   G   Q   T   V   V   M   I   S    224
781  TCG CTG ATA TGC ATG GTT CTA ACG ATC GCC GTA TAC CTC TTC GTC AAG AAA CTA CAA AAC
      S   L   I   C   M   V   L   T   I   A   V   Y   L   F   V   K   K   L   Q   N    244
841  TTG CAT GGA AAA TGC TTC ATC TGC TAC ATG GTG TGT CTC TTT ATG GGA TAT CTT TTC CTA
      L   H   G   K   C   F   I   C   Y   M   V   C   L   F   M   G   Y   L   F   L    264
901  TTG CTC GAT TTG TGG CAG ATA TCC ATT AGC TTT TGC AAA CCA GCA GGT TTT CTG GGT TAC
      L   L   D   L   W   Q   I   S   I   S   F   C   K   P   A   G   F   L   G   Y    284
```

FIG. 3B-1

```
961 TTC TTT GTC ATG GCC GCA TTT TTT TGG CTT TCC GTC ATC AGT CTG CAC CTT TGG AAC ACG
      F   F   V   M   A   A   F   F   W   L   S   V   I   S   L   H   L   W   N   T  304
1021 TTC AGA GGC TCC TCC CAC AAA GCG AAT CGC TTC TTA TTT GAG CAT CGG TTT CTG GCC TAC
      F   R   G   S   S   H   K   A   N   R   F   L   F   E   H   R   F   L   A   Y  324
1081 AAT ACC TAT GCT TGG GGC ATG GCG GTG GTC CTG ACA GGA ATT ACC GTT CTG GCC GAT AAC
      N   T   Y   A   W   G   M   A   V   V   L   T   G   I   T   V   L   A   D   N  344
1141 ATC GTG GAA AAC CAG GAT TGG AAT CCT CGT GTG GGC CAC GAG GGA CAC TGT TGG ATA TAT
      I   V   E   N   Q   D   W   N   P   R   V   G   H   E   G   H   C   W   I   Y  364
1201 ACT CAA GCC TGG TCA GCC ATG CTC TAC TTT TAC GGT CCA ATG GTA TTT CTT ATT GCC TTT
      T   Q   A   W   S   A   M   L   Y   F   Y   G   P   M   V   F   L   I   A   F  384
1261 AAC ATA ACC ATG TTC ATC CTG ACT GCT AAG CGT ATA TTA GGA GTG AAG AAG GAC ATT CAG
      N   I   T   M   F   I   L   T   A   K   R   I   L   G   V   K   K   D   I   Q  404
1321 AAC TTT GCG CAC AGG CAA GAG AGA AAG CAG AAG CTG AAC TCC GAC AAA CAG ACT TAC ACC
      N   F   A   H   R   Q   E   R   K   Q   K   L   N   S   D   K   Q   T   Y   T  424
1381 TTC TTC CTA CGG CTC TTC ATC ATT ATG GGA TTG TCC TGG AGC TTG GAG ATA GGC TCC TAC
      F   F   L   R   L   F   I   I   M   G   L   S   W   S   L   E   I   G   S   Y  444
1441 TTT TCG CAA TCC AAC CAA ACT TGG GCC AAC GTC TTT CTG GTG GCT GAC TAT TTA AAT TGG
      F   S   Q   S   N   Q   T   W   A   N   V   F   L   V   A   D   Y   L   N   W  464
1501 TCT CAA GGA ATC ATC ATA TTT ATA CTG TTC GTT CTG AAG CGC AGC ACG TGG AGA CTC TTG
      S   Q   G   I   I   I   F   I   L   F   V   L   K   R   S   T   W   R   L   L  484
1561 CAG GAG AGC ATT AGG GGG GAG GGT GAG GAG GTA AAC AAC AGT GAG GAA GAG ATT TCG CTA
      Q   E   S   I   R   G   E   G   E   E   V   N   N   S   E   E   E   I   S   L  504
1621 GAA AAC ACG ACG ACA CGA AAT GTC CTA TTA TAG                                      514
      E   N   T   T   T   R   N   V   L   L   *
1654 GAACCATCCTAAATCCACGAGGAGTGTCATTTCTAACAGATCTATGGCAAGTCGTATTACCGTGGGAACAACTCCTAAA
1733 AATAAAGCACGGAACTCGCCATTGGCTTAAAAGCTGTAATAAGTATATGTTTGTATCTTATTAATATTCAAACCATAAA
1812 TAACGGTTTCTGTATATCACTTTTCTTAAAACTATTCAACTAACTCAGATGGATTTAACACCGTTTATTGAACATAAGA
1891 TGTTTTTTAACATTTGAAATAAAAAATAATACTGCAATAAAGAAAAAAAAAAAAAAAA
```

FIG. 3B-2

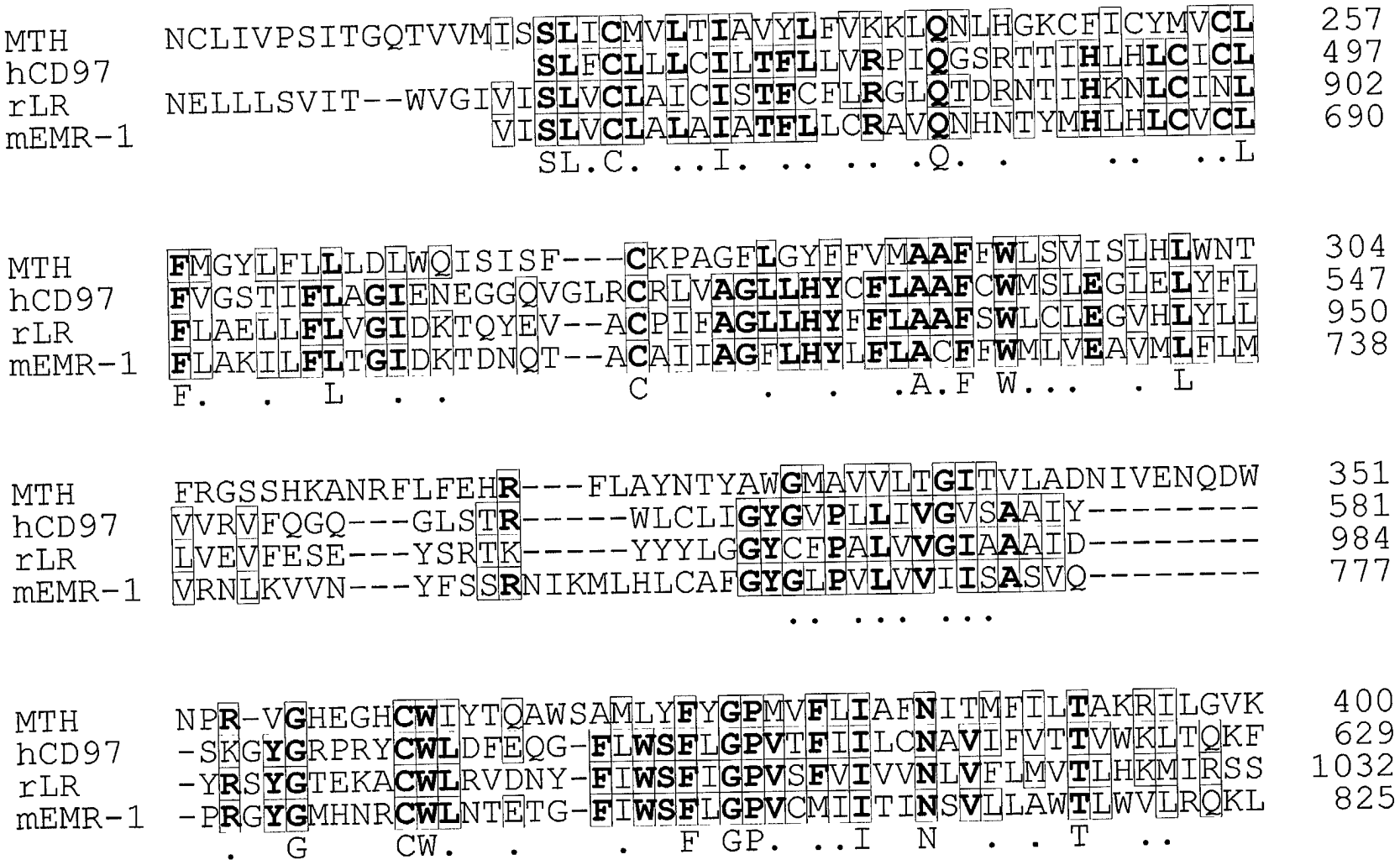
MTH NCLIVPSITGQTVVMISSLICMVLTIAVYLFVKKLQNLHGKCFICYMVCL 257
hCD97 SLFCLLLCILTFLLVRPIQGSRTTIHLHLLCICL 497
rLR NELLLSVIT--WVGIVISLVCLAICISTFCFLRGLQTDRNTIHKNLCINL 902
mEMR-1 VISLVCLALAIATFLLCRAVQNHNTYMHLHLCVCL 690
SL.C. ..I. .. .. .Q. L
MTH FMGYLFLLLDLWQISISF---CKPAGFLGYFFVMAAFFWLSVISLHLWNT 304
hCD97 FVGSTIFLAGIENEGGQVGLRCRLVAGLLHYCFLAAFCWMSLEGLELYFL 547
rLR FLAELLFLVGIDKTQYEV--ACPIFAGLLHYFFLAAFSWLCLEGVHLYLL 950
mEMR-1 FLAKILFLTGIDKTDNQT--ACAIIAGFLHYLFLACFFWMLVEAVMLFLM 738
F. . L . . C . . .A.F W... . L
MTH FRGSSHKANRFLFEHR---FLAYNTYAWGMAVVLTGITVLADNIVENQDW 351
hCD97 VVRVFQGQ---GLSTR-----WLCLIGYGVPLLIVGVSAAIY-------- 581
rLR LVEVFESE---YSRTK-----YYYLGGYCFPALVVGIAAAID-------- 984
mEMR-1 VRNLKVVN---YFSSRNIKMLHLCAFGYGLPVLVVIISASVQ-------- 777
.. ..
MTH NPR-VGHEGHCWIYTQAWSAMLYFYGPMVFLIAFNITMFILTAKRILGVK 400
hCD97 -SKGYGRPRYCWLDFEQG-FLWSFLGPVTFIILCNAVIFVTTVWKLTQKF 629
rLR -YRSYGTEKACWLRVDNY-FIWSFIGPVSFVIVVNLVFLMVTLHKMIRSS 1032
mEMR-1 -PRGYGMHNRCWLNTETG-FIWSFLGPVCMIITINSVLLAWTLWVLRQKL 825
. G CW. . . F GP. ..I N . . T ..

FIG. 4A

```
MTH       KDIQNFAHRQERKQKLNSDKQTYTFFLRLFIIMGLSWSLEIGSYFSQSNQ    450
hCD97     SEIN-----PDMKKLKKARALTITAIAQLFLL-GCTWVFGLFIFDDRS--    671
rLR       SVLK-----PDSSRLDNIKSWALGAIALLFLL-GLTWAFGLLFINKES--   1074
mEMR-1    CSVS-----SEVSKLKDTRLLTFKAIAQIFIL-GCSWVLGIFQIGPLA--    867
                      .       .  .   ..  .      .LF.L G .W   .        S

MTH       TWANVFLVADYLNWSQGIIIFILFVL
hCD97     --LVLTYVFTILNCLQGAFLYLLHCL
rLR       --VVMAYLFTTFFNAFQGVFIFV
mEMR-1    --SIMAYLFTIINSLQGAFIFLIHCL
                .  .    .N  QG  ....   L
```

FIG. 4B

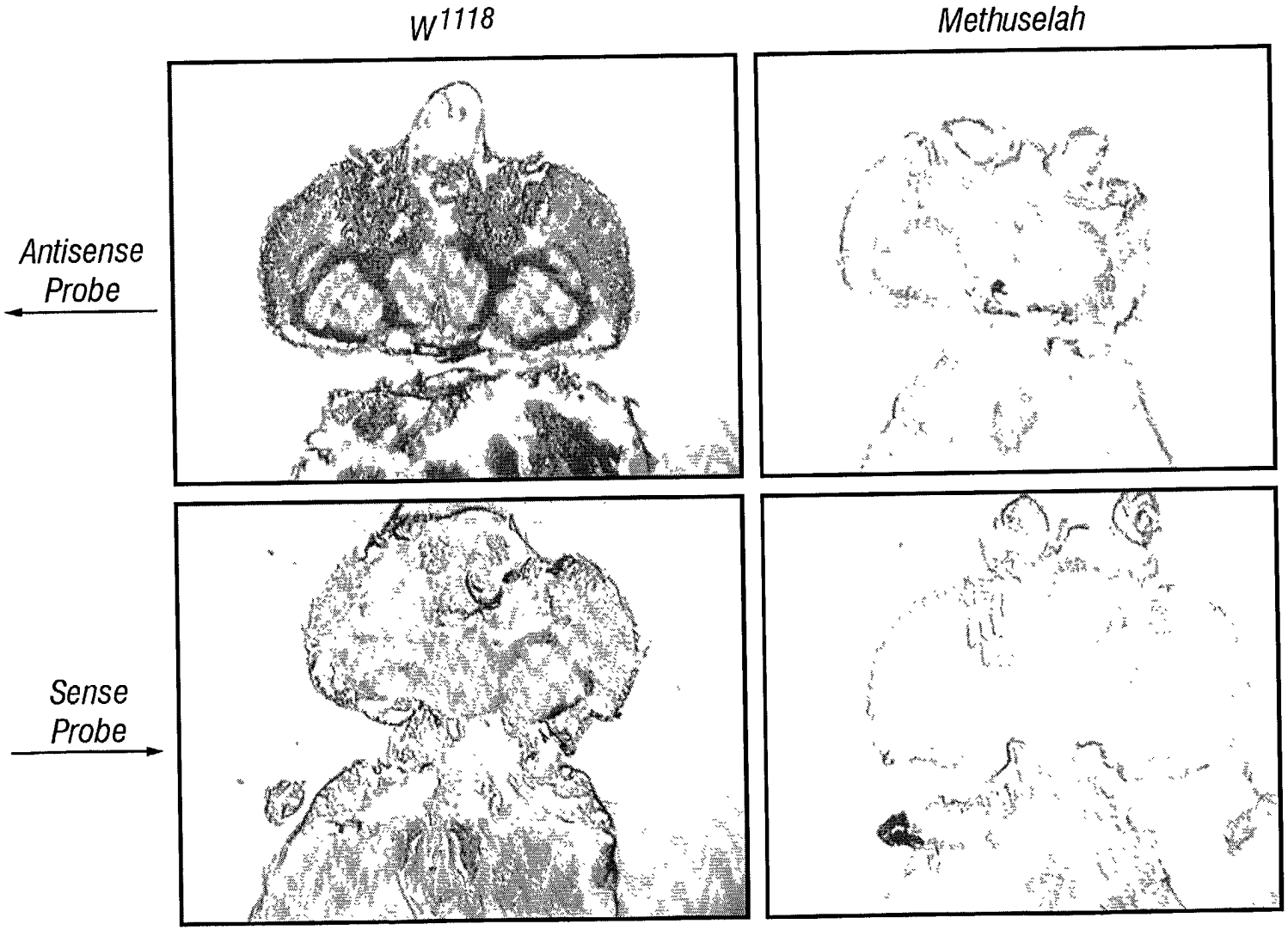

FIG. 5

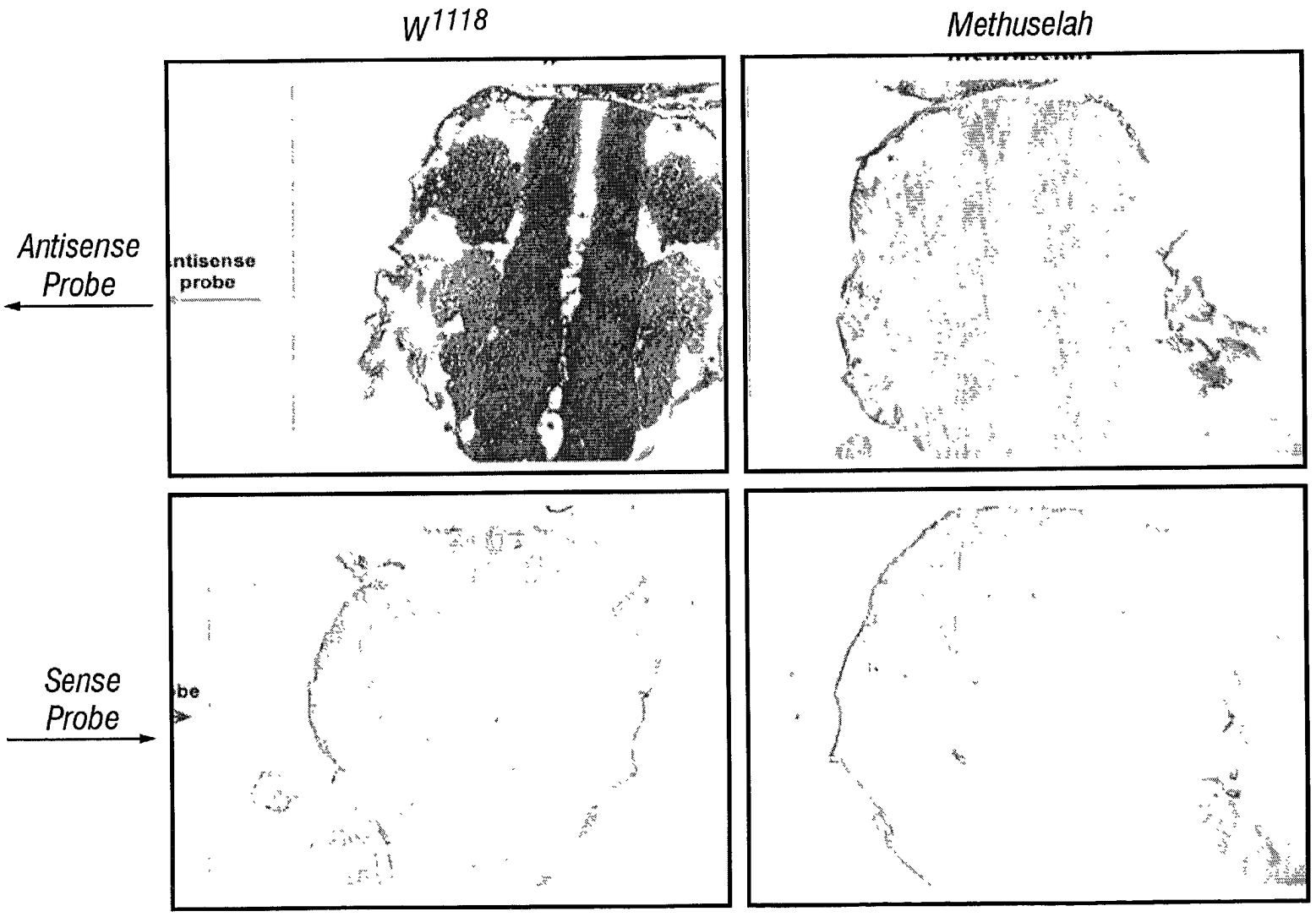

FIG. 6

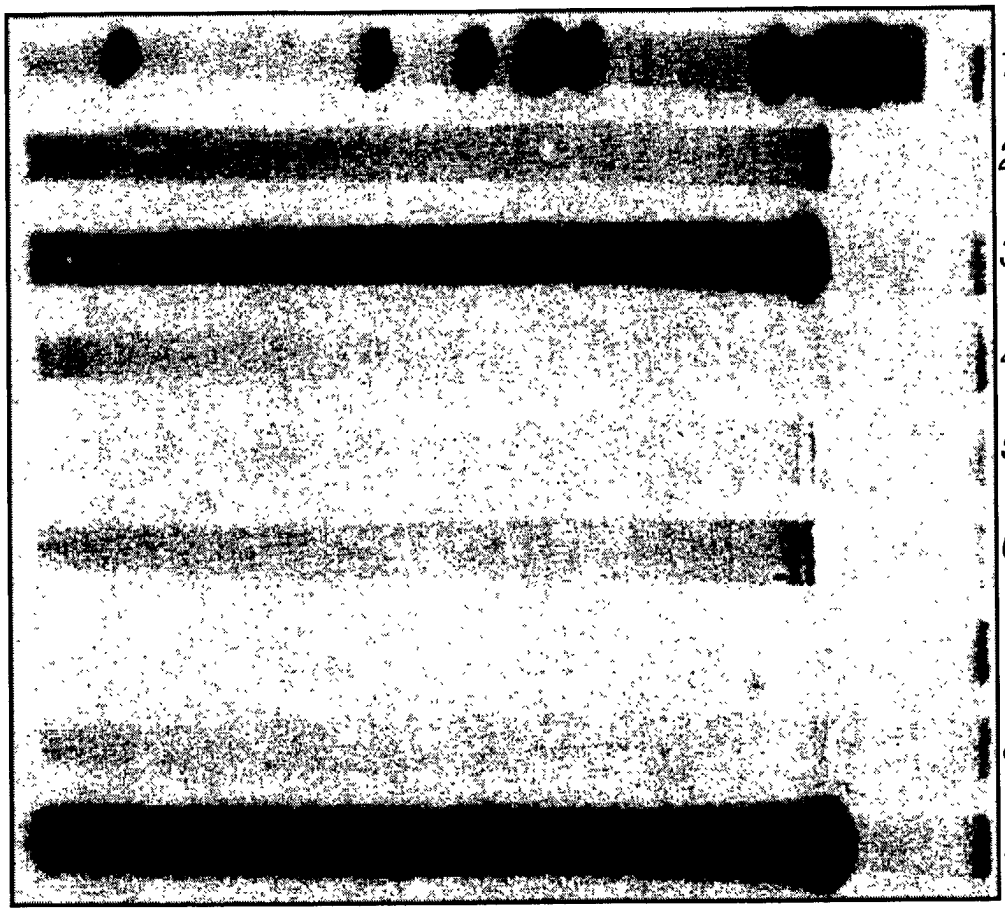

FIG. 7

FIG. 8A

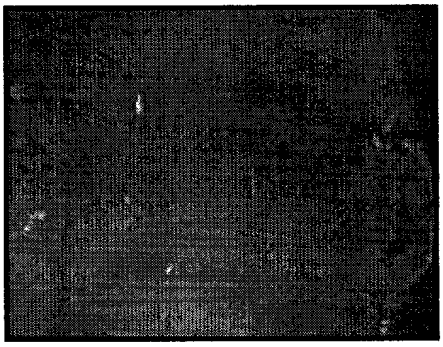

FIG. 8B

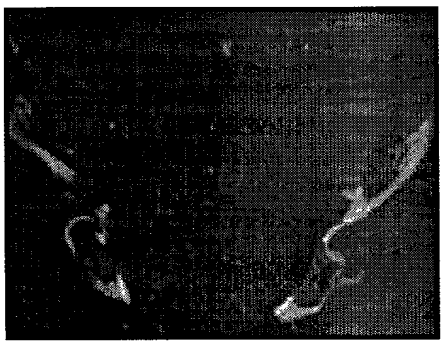

FIG. 8C

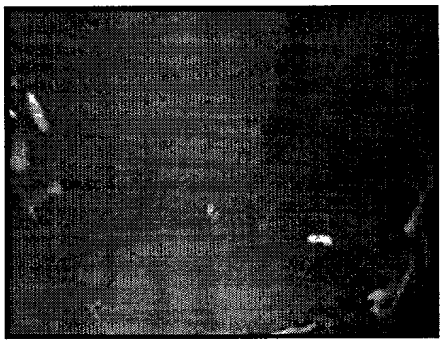

FIG. 8D

FIG. 8E

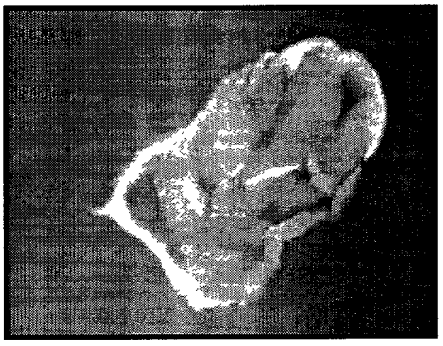

FIG. 8F

FIG. 8G

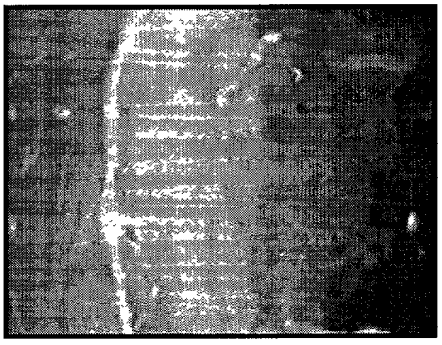

FIG. 8H